



wwPDB EM Validation Summary Report ⓘ

Jul 3, 2024 – 01:03 pm BST

PDB ID : 7OH3
EMDB ID : EMD-12892
Title : Nog1-TAP associated immature ribosomal particle population B from *S. cerevisiae*
Authors : Milkereit, P.; Poell, G.
Deposited on : 2021-05-08
Resolution : 3.40 Å (reported)
Based on initial model : 3JCT

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

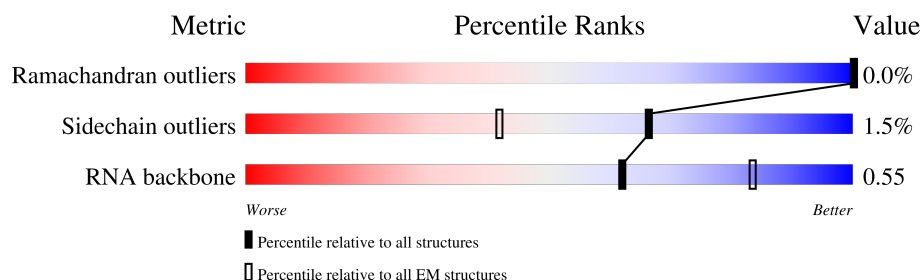
EMDB validation analysis : 0.0.1.dev92
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.37.1

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.40 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	1	3396	
2	2	158	
3	3	121	
4	5	120	
5	A	254	
6	B	387	
7	C	362	
8	D	297	

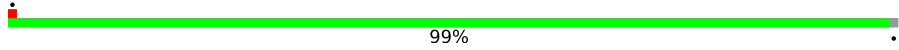

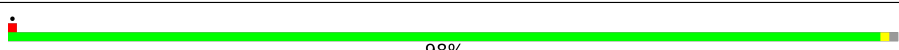
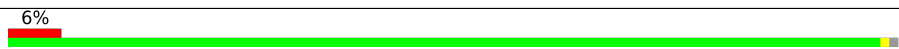
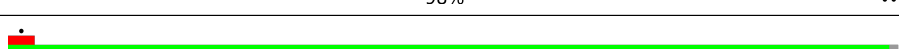
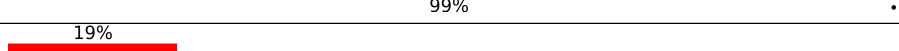
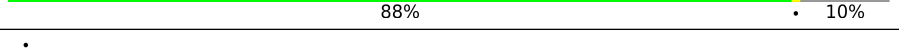
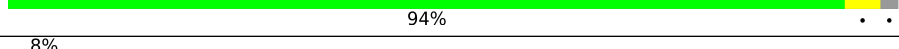
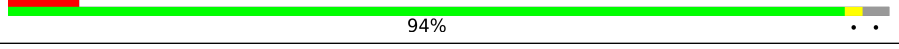
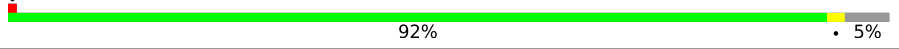


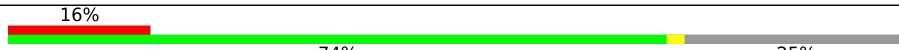


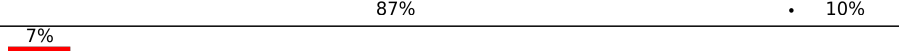
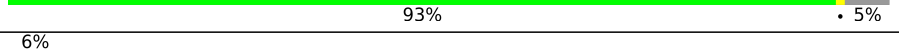
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Mol	Chain	Length	Quality of chain
9	E	176	
10	F	244	
11	G	256	
12	H	191	
13	J	174	
14	L	199	
15	M	138	
16	N	204	
17	O	199	
18	P	184	
19	Q	186	
20	R	189	
21	S	172	
22	T	160	
23	U	121	
24	V	137	
25	W	236	
26	X	142	
27	Y	127	
28	Z	136	
29	a	149	
30	b	647	
31	c	105	
32	d	113	
33	e	130	

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Mol	Chain	Length	Quality of chain
34	f	107	
35	g	121	
36	h	120	
37	i	100	
38	j	88	
39	k	78	
40	l	51	
41	m	486	
42	p	92	
43	r	261	
44	s	520	
45	u	199	
46	v	344	
47	w	203	
48	x	515	
49	y	245	
50	z	106	

2 Entry composition [i](#)

There are 52 unique types of molecules in this entry. The entry contains 240945 atoms, of which 104342 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called 25S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	1	3013	Total	C	H	N	O	P	0	0
			96890	28804	32398	11667	21009	3012		

- Molecule 2 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	2	155	Total	C	H	N	O	P	0	0
			4957	1473	1664	580	1085	155		

- Molecule 3 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	3	121	Total	C	H	N	O	P	0	0
			3883	1152	1304	461	845	121		

- Molecule 4 is a protein called rRNA-processing protein CGR1.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	5	73	Total	C	H	N	O	S	0	0
			1334	395	689	133	114	3		

- Molecule 5 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	A	196	Total	C	H	N	O		0	0
			3098	954	1579	301	264			

- Molecule 6 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms						AltConf	Trace
6	B	386	Total	C	H	N	O	S	0	0
			6247	1956	3166	584	533	8		

- Molecule 7 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	C	352	Total	C	H	N	O	S	0	0
			5490	1691	2804	509	483	3		

- Molecule 8 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	D	267	Total	C	H	N	O	S	0	0
			4266	1361	2114	379	410	2		

- Molecule 9 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
9	E	156	Total	C	H	N	O	S	0	0
			2567	800	1328	222	216	1		

- Molecule 10 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
10	F	222	Total	C	H	N	O	S	0	0
			3647	1151	1863	324	308	1		

- Molecule 11 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
11	G	228	Total	C	H	N	O	S	0	0
			3668	1142	1884	320	319	3		

- Molecule 12 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
12	H	188	Total	C	H	N	O	S	0	0
			3059	948	1566	271	270	4		

- Molecule 13 is a protein called 60S ribosomal protein L11-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
13	J	169	Total	C	H	N	O	S	0	0
			2738	847	1385	253	249	4		

- Molecule 14 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	L	187	Total	C	H	N	O	0	0
			3057	934	1558	307	258		

- Molecule 15 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace	
15	M	137	Total	C	H	N	O	S	0	0
			2214	678	1155	200	179	2		

- Molecule 16 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
16	N	203	Total	C	H	N	O	S	0	0
			3500	1077	1780	361	281	1		

- Molecule 17 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
17	O	197	Total	C	H	N	O	S	0	0
			3216	1003	1661	289	262	1		

- Molecule 18 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	P	174	Total	C	H	N	O	0	0
			2798	857	1419	276	246		

- Molecule 19 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
19	Q	134	Total	C	H	N	O	S	0	0
			2151	659	1116	196	179	1		

- Molecule 20 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	R	156	Total	C	H	N	O	0	0
			2601	781	1343	265	212		

- Molecule 21 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
21	S	171	Total	C	H	N	O	S	0	0
			2913	925	1476	266	243	3		

- Molecule 22 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
22	T	113	Total	C	H	N	O	S	0	0
			1868	574	962	172	157	3		

- Molecule 23 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
23	U	98	Total	C	H	N	O		0	0
			1571	502	796	128	145			

- Molecule 24 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
24	V	136	Total	C	H	N	O	S	0	0
			2052	628	1049	189	179	7		

- Molecule 25 is a protein called Ribosome assembly factor MRT4.

Mol	Chain	Residues	Atoms						AltConf	Trace
25	W	234	Total	C	H	N	O	S	0	0
			3806	1194	1921	323	362	6		

- Molecule 26 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms						AltConf	Trace
26	X	117	Total	C	H	N	O	S	0	0
			1932	602	995	164	169	2		

- Molecule 27 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
27	Y	126	Total	C	H	N	O		0	0
			2075	625	1082	192	176			

- Molecule 28 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	Z	135	Total	C	H	N	O	0	0
			2248	710	1156	202	180		

- Molecule 29 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms						AltConf	Trace
29	a	93	Total	C	H	N	O	S	0	0
			1512	479	777	130	125	1		

- Molecule 30 is a protein called Nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace	
30	b	455	Total	C	H	N	O	S	0	0
			7450	2353	3755	640	684	18		

- Molecule 31 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms						AltConf	Trace
31	c	97	Total	C	H	N	O	S	0	0
			1541	479	798	124	139	1		

- Molecule 32 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
32	d	105	Total	C	H	N	O	S	0	0
			1761	544	905	163	148	1		

- Molecule 33 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace	
33	e	127	Total	C	H	N	O	S	0	0
			2111	647	1091	205	167	1		

- Molecule 34 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
34	f	106	Total	C	H	N	O	S	0	0
			1731	540	881	165	144	1		

- Molecule 35 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
35	g	112	Total	C	H	N	O	S	0	0
			1831	546	950	179	152	4		

- Molecule 36 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
36	h	119	Total	C	H	N	O	S	0	0
			2048	615	1079	186	167	1		

- Molecule 37 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
37	i	99	Total	C	H	N	O	S	0	0
			1621	481	850	156	132	2		

- Molecule 38 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
38	j	87	Total	C	H	N	O	S	0	0
			1369	414	688	148	114	5		

- Molecule 39 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms						AltConf	Trace
39	k	70	Total	C	H	N	O	S	0	0
			1197	362	634	106	95			

- Molecule 40 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms						AltConf	Trace
40	l	50	Total	C	H	N	O	S	0	0
			912	272	476	97	65	2		

- Molecule 41 is a protein called Nucleolar GTP-binding protein 2.

Mol	Chain	Residues	Atoms						AltConf	Trace
41	m	469	Total	C	H	N	O	S	0	0
			7611	2381	3837	685	699	9		

- Molecule 42 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
42	p	87	Total	C	H	N	O	S	0	0
			1375	411	710	134	115	5		

- Molecule 43 is a protein called Ribosome biogenesis protein NSA2.

Mol	Chain	Residues	Atoms						AltConf	Trace
43	r	230	Total	C	H	N	O	S	0	0
			3827	1177	1967	352	324	7		

- Molecule 44 is a protein called Nuclear GTP-binding protein NUG1.

Mol	Chain	Residues	Atoms						AltConf	Trace
44	s	54	Total	C	H	N	O	S	0	0
			947	279	503	90	73	2		

- Molecule 45 is a protein called Ribosome biogenesis protein RLP24.

Mol	Chain	Residues	Atoms						AltConf	Trace
45	u	150	Total	C	H	N	O	S	0	0
			2582	793	1317	253	210	9		

- Molecule 46 is a protein called Ribosome biogenesis protein RPF2.

Mol	Chain	Residues	Atoms						AltConf	Trace
46	v	287	Total	C	H	N	O	S	0	0
			4718	1482	2400	408	412	16		

- Molecule 47 is a protein called Regulator of ribosome biosynthesis.

Mol	Chain	Residues	Atoms						AltConf	Trace
47	w	182	Total	C	H	N	O	S	0	0
			2960	911	1512	261	271	5		

- Molecule 48 is a protein called Ribosome assembly protein 4.

Mol	Chain	Residues	Atoms						AltConf	Trace
48	x	488	Total	C	H	N	O	S	0	0
			7606	2398	3799	677	711	21		

- Molecule 49 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms						AltConf	Trace
49	y	244	Total	C	H	N	O	S	0	0
			3685	1146	1836	319	377	7		

- Molecule 50 is a protein called UPF0642 protein YBL028C.

Mol	Chain	Residues	Atoms						AltConf	Trace
50	z	42	Total	C	H	N	O		0	0
			699	206	364	69	60			


- Molecule 51 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
51	b	1	Total	Mg	0
			1	1	
51	m	1	Total	Mg	0
			1	1	

- Molecule 52 is ZINC ION (three-letter code: ZN) (formula: Zn).


Mol	Chain	Residues	Atoms		AltConf
52	j	1	Total	Zn	0
			1	1	
52	p	1	Total	Zn	0
			1	1	
52	u	1	Total	Zn	0
			1	1	

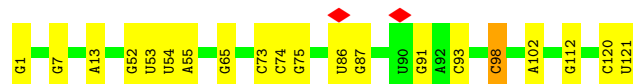
U3304	A3142	G2952	U2842	G2622	A2523	A2242	A1750
A3316	U2953	U2953	U2843	G2623	A2524	A2243	G1751
U3319	U2954	U2954	C2844	G2624	A2525	A2244	C1761
U3334	U2955	A2956	U	A2626	C2526	U	C
A3335	U3154	U	A2847	A2635	G2530	G2247	U
U3341	U	U3985	C2857	A2636	C2531	C2248	U
A3342	U3157	C2970	U2858	A2637	U2532	G2249	U1765
A3343	G3158	A2971	U	A2638	G2533	G2250	U1766
G3344	A3165	G2972	U2860	U2641	G2534	A2252	G1770
G3345	A3172	U2977	U2861	A2642	U2537	A2255	G1796
C3350	G3173	U	U2862	A2643	C	A	A1797
U3351	A3174	U2979	A2863	C	U2538	U	G1807
U3352	U3175	U2980	A2864	G2645	A2540	A	G1808
G3353	G3176	U2981	U2865	U2651	U2541	U2260	G1812
U	G3179	U2982	U2866	G2651	U2542	G2261	A1813
G3356	U3180	C2983	C2867	U2652	U2543	A2262	A1814
C3360	A3181	U2986	U2868	C2653	U2544	U2263	U1815
C3368	G3187	G2987	G2870	U2654	C2545	U2264	A1816
U3369	U3195	G3003	G2871	U2655	A2547	U	G1817
U3396	U3196	A3012	A2872	A2656	G2548	U2268	U1820
A3375	U3197	A3017	U2873	A2657	U2549	U2269	U1821
C3378	U3198	A3021	G2874	G2658	U2550	A2270	U
U3389	U3207	G3022	U2875	G2659	U2551	A2271	U
C3398	A3213	U3023	U2876	A2667	C2552	G2272	U
U3396	C3217	G3026	G2877	A2674	U2553	G2273	A1839
A3396	A3218	A3027	C2878	G2677	A2554	U2274	A1841
C3228	G3219	G3029	C2879	U2678	G2555	C2277	A1842
G3229	C3219	A3031	U2887	U2679	A2561	A2278	C1849
A3245	A3245	A3032	U2888	U2680	A2562	A2279	C1857
G3246	G3246	U3058	C2889	A2681	C2568	A2280	A1858
G3247	G3247	G3059	U2890	U2682	A	A	A1859
G3253	G3253	U3078	U2891	A2683	U	U	G1863
U3259	U3259	A3079	U2892	A2684	U2571	U2191	C1866
G3260	G3260	A3086	A2802	G2686	C2572	C2192	U
U3269	U3269	C3092	A2803	U2587	G2573	G2194	G1878
A3273	A3273	U3100	C2810	U2588	G2574	C2196	A1879
G3276	G3276	G3101	U2817	A2702	G2575	C2197	U1880
U3281	U3281	A3109	U2818	A2703	U2576	A2198	G1906
U3287	U3287	A3129	U2819	A2704	U2577	C2204	A1909
		U3131	A2820	U2712	U2578	U2205	U1937
			U2821	U2713	U2579	G2206	G1952
			U2822	U2714	U2580	A2207	G1953
			U2823	U2715	U2581	A2208	U
			U2824	U2716	U2582	U2209	A
			U2825	U2717	U2583	G2210	U
			U2826	U2718	U2584	A2223	G
			U2827	U2719	U2585	A2224	U
			U2828	U2720	U2586		
			U2829	U2721	U2587		
			U2830	U2722	U2588		
			U2831	U2723	U2589		
			U2832	U2724	U2590		
			U2833	U2725	U2591		
			U2834	U2726	U2592		
			U2835	U2727	U2593		
			U2836	U2728	U2594		
			U2837	U2729	U2595		
			U2838	U2730	U2596		
			U2839	U2731	U2597		
			U2840	U2732	U2598		
			U2841	U2733	U2599		
			U2842	U2734	U2600		
			U2843	U2735	U2601		
			U2844	U2736	U2602		
			U2845	U2737	U2603		
			U2846	U2738	U2604		
			U2847	U2739	U2605		
			U2848	U2740	U2606		
			U2849	U2741	U2607		
			U2850	U2742	U2608		
			U2851	U2743	U2609		
			U2852	U2744	U2610		
			U2853	U2745	U2611		
			U2854	U2746	U2612		
			U2855	U2747	U2613		
			U2856	U2748	U2614		
			U2857	U2749	U2615		
			U2858	U2750	U2616		
			U2859	U2751	U2617		
			U2860	U2752	U2618		
			U2861	U2753	U2619		
			U2862	U2754	U2620		
			U2863	U2755	U2621		
			U2864	U2756	U2622		
			U2865	U2757	U2623		
			U2866	U2758	U2624		
			U2867	U2759	U2625		
			U2868	U2760	U2626		
			U2869	U2761	U2627		
			U2870	U2762	U2628		
			U2871	U2763	U2629		
			U2872	U2764	U2630		
			U2873	U2765	U2631		
			U2874	U2766	U2632		
			U2875	U2767	U2633		
			U2876	U2768	U2634		
			U2877	U2769	U2635		
			U2878	U2770	U2636		
			U2879	U2771	U2637		
			U2880	U2772	U2638		
			U2881	U2773	U2639		
			U2882	U2774	U2640		
			U2883	U2775	U2641		
			U2884	U2776	U2642		
			U2885	U2777	U2643		
			U2886	U2778	U2644		
			U2887	U2779	U2645		
			U2888	U2780	U2646		
			U2889	U2781	U2647		
			U2890	U2782	U2648		
			U2891	U2783	U2649		
			U2892	U2784	U2650		
			U2893	U2785	U2651		
			U2894	U2786	U2652		
			U2895	U2787	U2653		
			U2896	U2788	U2654		
			U2897	U2789	U2655		
			U2898	U2790	U2656		
			U2899	U2791	U2657		
			U2900	U2792	U2658		
			U2901	U2793	U2659		
			U2902	U2794	U2660		
			U2903	U2795	U2661		
			U2904	U2796	U2662		
			U2905	U2797	U2663		
			U2906	U2798	U2664		
			U2907	U2799	U2665		
			U2908	U2800	U2666		
			U2909	U2801	U2667		
			U2910	U2802	U2668		
			U2911	U2803	U2669		
			U2912	U2804	U2670		
			U2913	U2805	U2671		
			U2914	U2806	U2672		
			U2915	U2807	U2673		
			U2916	U2808	U2674		
			U2917	U2809	U2675		
			U2918	U2810	U2676		
			U2919	U2811	U2677		
			U2920	U2812	U2678		
			U2921	U2813	U2679		
			U2922	U2814	U2680		
			U2923	U2815	U2681		
			U2924	U2816	U2682		
			U2925	U2817	U2683		
			U2926	U2818	U2684		
			U2927	U2819	U2685		
			U2928	U2820	U2686		
			U2929	U2821	U2687		
			U2930	U2822	U2688		
			U2931	U2823	U2689		
			U2932	U2824	U2690		
			U2933	U2825	U2691		
			U2934	U2826	U2692		
			U2935	U2827	U2693		
			U2936	U2828	U2694		
			U2937	U2829	U2695		
			U2938	U2830	U2696		
			U2939	U2831	U2697		
			U2940	U2832	U2698		
			U2941	U2833	U2699		
			U2942	U2834	U2700		
			U2943	U2835	U2701		
			U2944	U2836	U2702		
			U2945	U2837	U2703		
			U2946	U2838	U2704		
			U2947	U2839	U2705		
			U2948	U2840	U2706		
			U2949	U2841	U2707		
			U2950	U2842	U2708		
			U2951	U2843	U2709		
			U2952	U2844	U2710		
			U2953	U2845	U2711		
			U2954	U2846	U2712		
			U2955	U2847	U2713		
			U2956	U2848	U2714		
			U2957	U2849	U2715		
			U2958	U2850	U2716		
			U2959	U2851	U2717		
			U2960	U2852	U2718		
			U2961	U2853	U2719		
			U2962	U2854	U2720		
			U2963	U2855	U2721		
			U2964	U2856	U2722		
			U2965	U2857	U2723		
			U2966	U2858	U2724		
			U2967	U2859	U2725		
			U2968	U2860	U2726		
			U2969	U2861	U2727		
			U2970	U2862	U2728		
			U2971	U2863	U2729		
			U2972	U2864	U2730		
			U2973	U2865	U2731		
			U2974	U2866	U2732		
			U2975	U2867	U2733		
			U2976	U2868	U2734		
			U2977	U2869	U2735		
			U2978	U2870	U2736		
			U2979	U2871	U2737		
			U2980	U2872	U2738		
			U2981	U2873	U2739		
			U2982	U2874			

Chain 2:  79% 18% ..



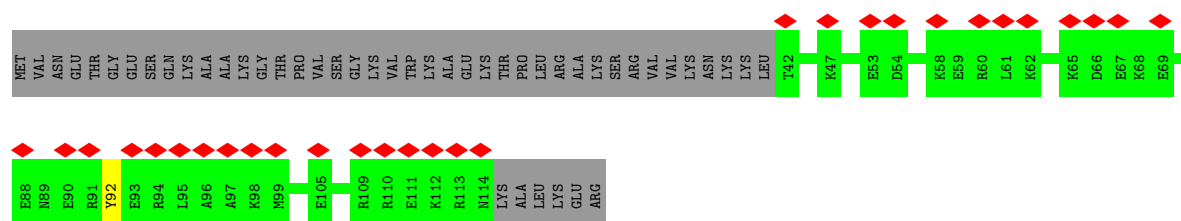
• Molecule 3: 5S rRNA

Chain 3:  83% 16% .




• Molecule 4: rRNA-processing protein CGR1

Chain 5:  24% 60% 39% .



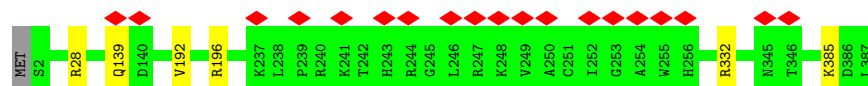
• Molecule 5: 60S ribosomal protein L2-A

Chain A:  77% 23%



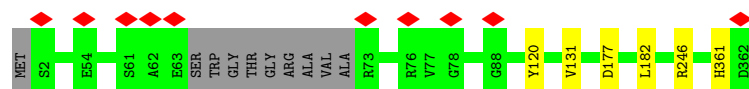
• Molecule 6: 60S ribosomal protein L3

Chain B:  5% 98% .



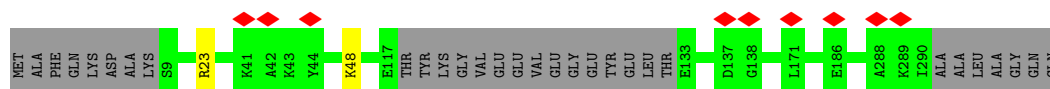
• Molecule 7: 60S ribosomal protein L4-A

Chain C:  96% ..




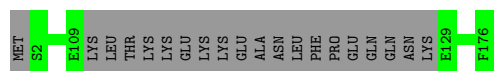
• Molecule 8: 60S ribosomal protein L5

Chain D:  89% 10%




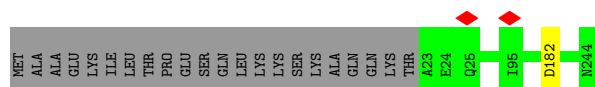
- Molecule 9: 60S ribosomal protein L6-A

Chain E:  89% 11%




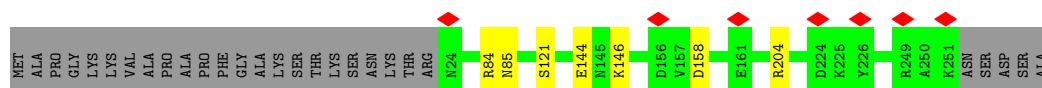
- Molecule 10: 60S ribosomal protein L7-A

Chain F:  91% 9%



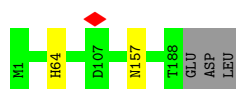
- Molecule 11: 60S ribosomal protein L8-A

Chain G:  86% 11%



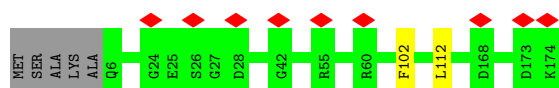
- Molecule 12: 60S ribosomal protein L9-A

Chain H:  97% ..

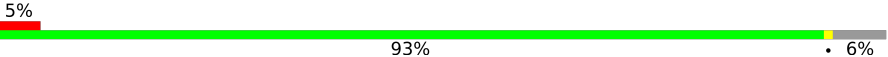


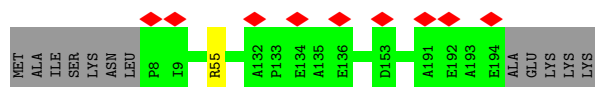
- Molecule 13: 60S ribosomal protein L11-A

Chain J:  5% 96% ..

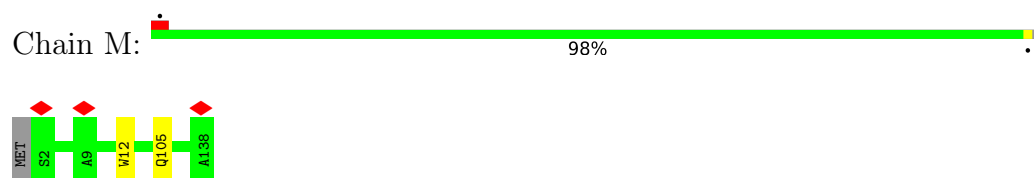


- Molecule 14: 60S ribosomal protein L13-A

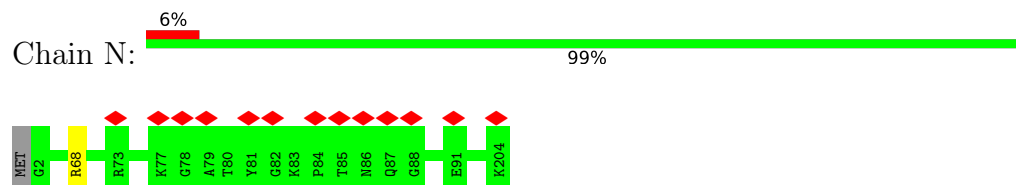
Chain L:  5% 93% 6%



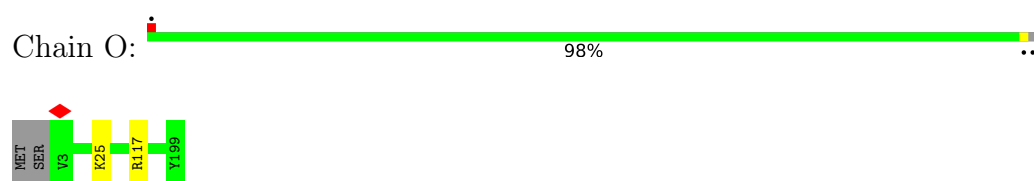
- Molecule 15: 60S ribosomal protein L14-A



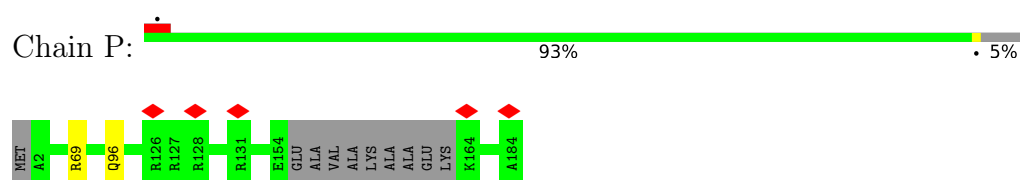
- Molecule 16: 60S ribosomal protein L15-A



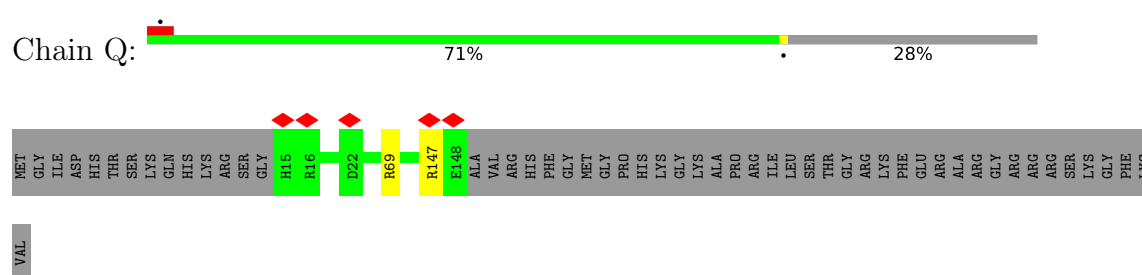
- Molecule 17: 60S ribosomal protein L16-A



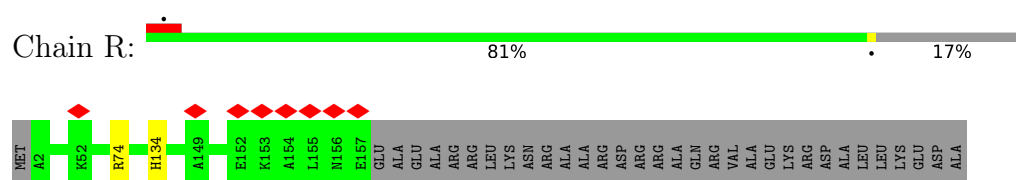
- Molecule 18: 60S ribosomal protein L17-A



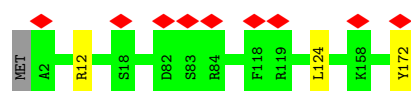
- Molecule 19: 60S ribosomal protein L18-A



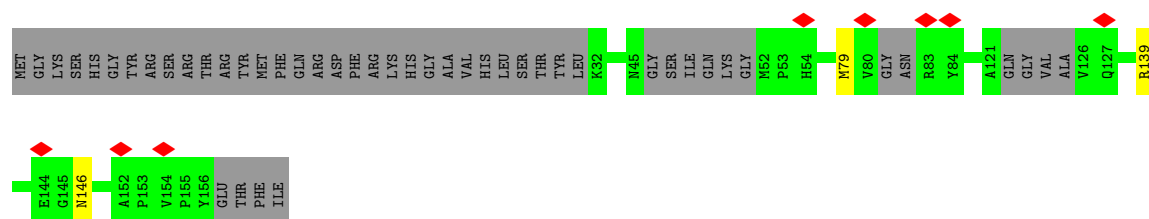
- Molecule 20: 60S ribosomal protein L19-A



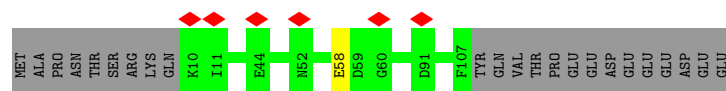
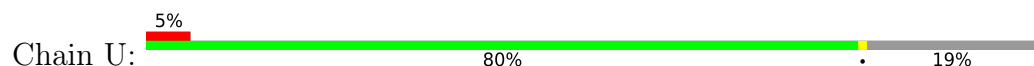
- Molecule 21: 60S ribosomal protein L20-A



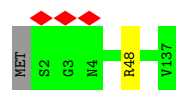
- Molecule 22: 60S ribosomal protein L21-A



- Molecule 23: 60S ribosomal protein L22-A



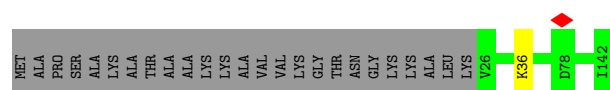
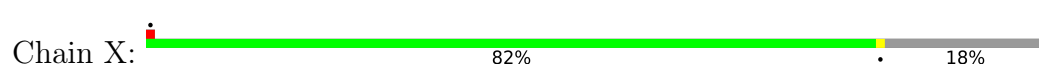
- Molecule 24: 60S ribosomal protein L23-A



- Molecule 25: Ribosome assembly factor MRT4



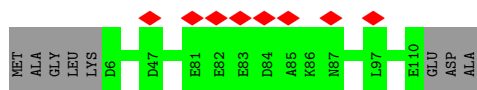
- Molecule 26: 60S ribosomal protein L25



- Molecule 27: 60S ribosomal protein L26-A

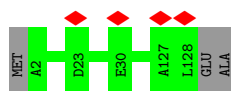






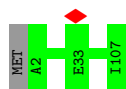
- Molecule 33: 60S ribosomal protein L32

Chain e: 98%



- Molecule 34: 60S ribosomal protein L33-A

Chain f: 99%



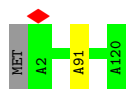
- Molecule 35: 60S ribosomal protein L34-A

Chain g: 5% 92% 7%



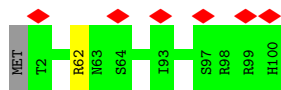
- Molecule 36: 60S ribosomal protein L35-A

Chain h: 98%



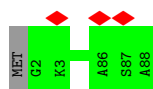
- Molecule 37: 60S ribosomal protein L36-A

Chain i: 6% 98% 7%

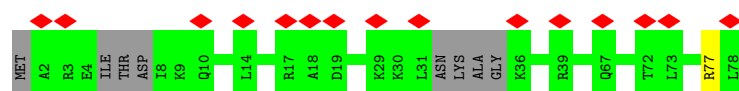
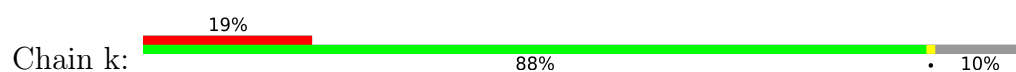


- Molecule 38: 60S ribosomal protein L37-A

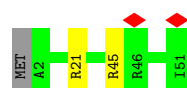
Chain j: 99%



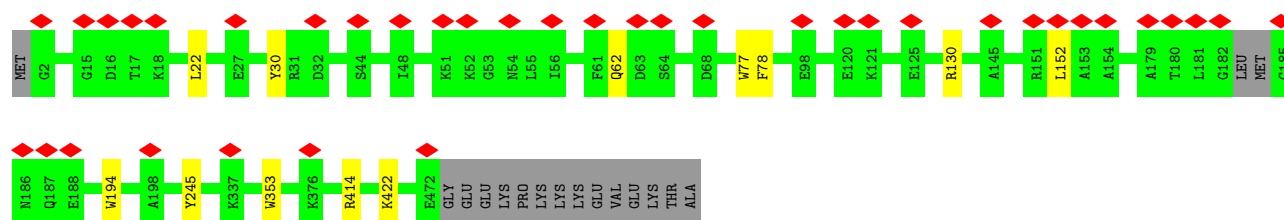
- Molecule 39: 60S ribosomal protein L38



- Molecule 40: 60S ribosomal protein L39



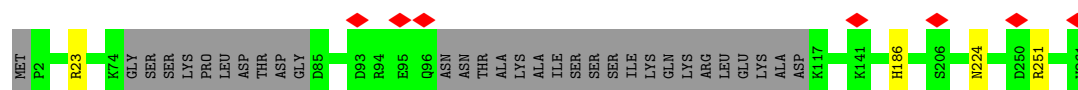
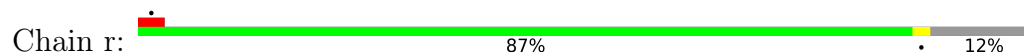
- Molecule 41: Nucleolar GTP-binding protein 2



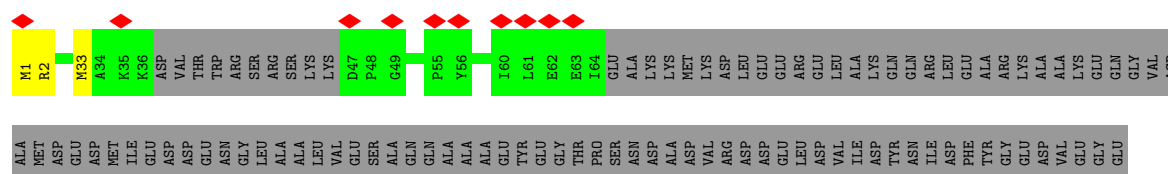
- Molecule 42: 60S ribosomal protein L43-A

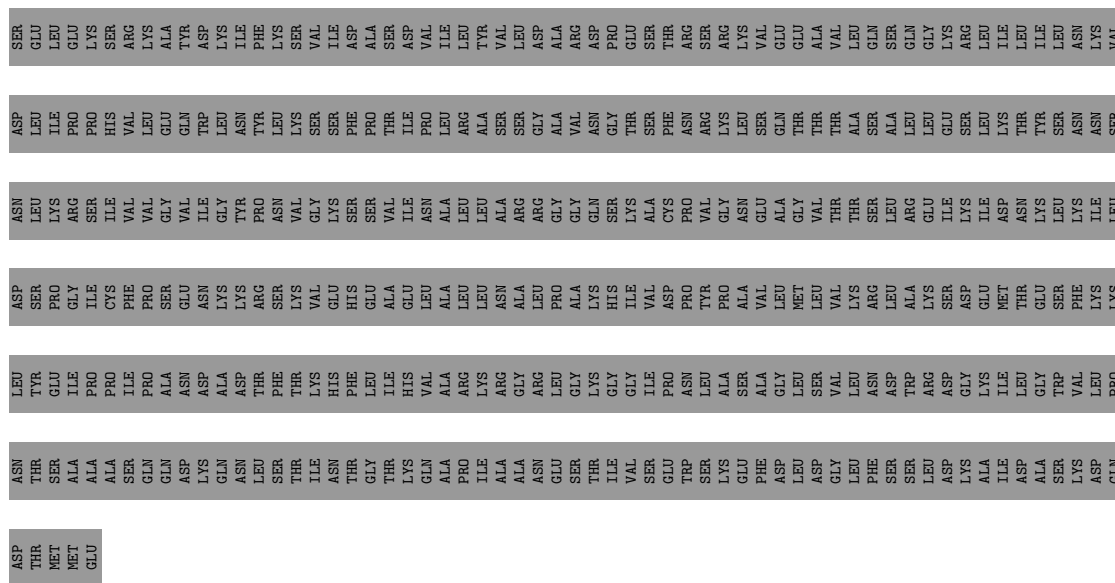


- Molecule 43: Ribosome biogenesis protein NSA2

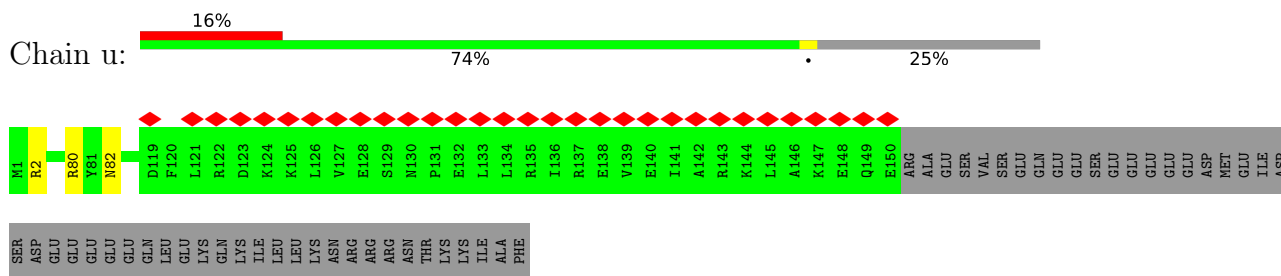


- Molecule 44: Nuclear GTP-binding protein NUG1

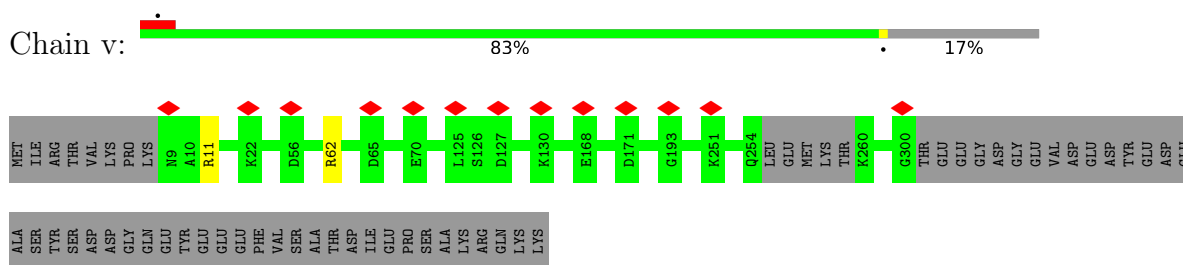




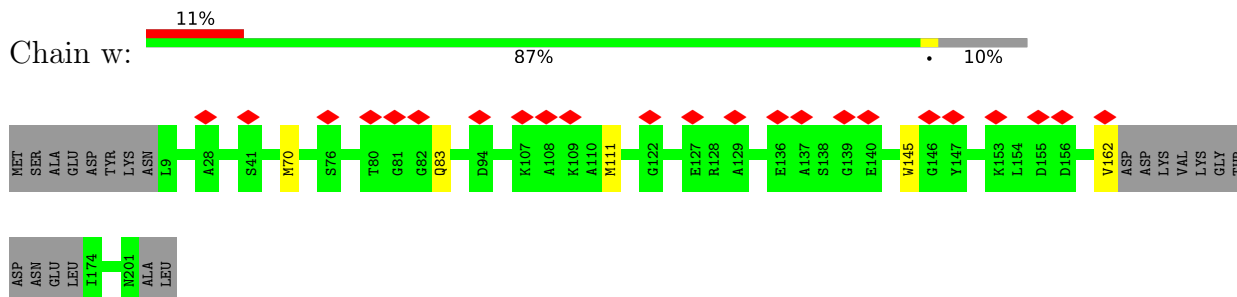
- Molecule 45: Ribosome biogenesis protein RLP24



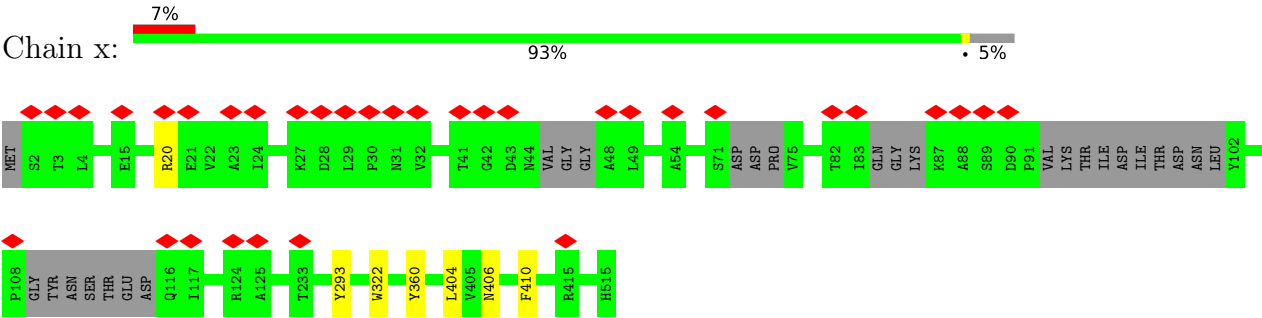
- Molecule 46: Ribosome biogenesis protein RPF2



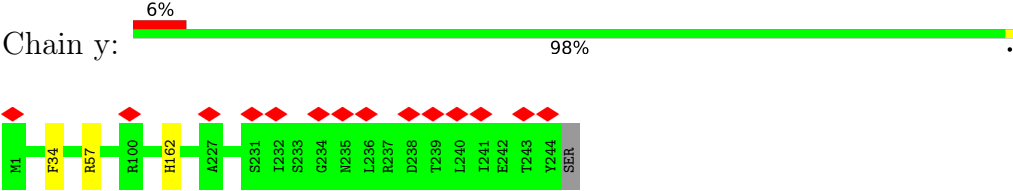
- Molecule 47: Regulator of ribosome biosynthesis



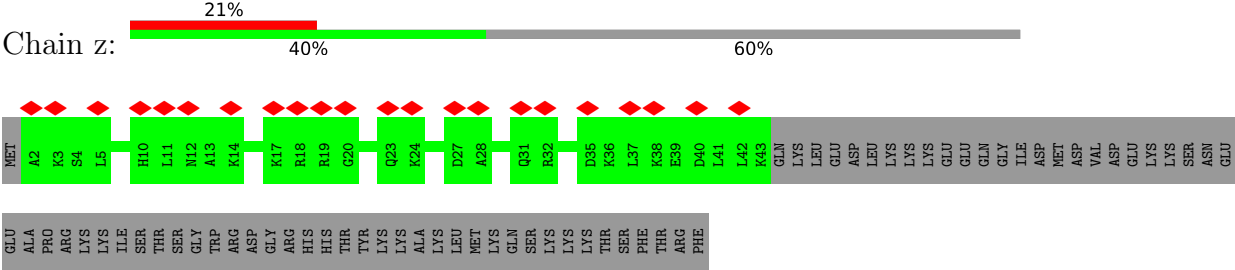
- Molecule 48: Ribosome assembly protein 4



• Molecule 49: Eukaryotic translation initiation factor 6



• Molecule 50: UPF0642 protein YBL028C



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	18823	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	84.67	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.136	Depositor
Minimum map value	-0.051	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.026	Depositor
Map size (Å)	425.40002, 425.40002, 425.40002	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.0635, 1.0635, 1.0635	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: MG, ZN

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	1	0.16	0/72171	0.74	44/112459 (0.0%)
2	2	0.16	0/3678	0.77	4/5722 (0.1%)
3	3	0.16	0/2883	0.78	6/4491 (0.1%)
4	5	0.24	0/649	0.37	0/848
5	A	0.24	0/1547	0.43	0/2079
6	B	0.24	0/3152	0.43	0/4239
7	C	0.24	0/2735	0.41	0/3700
8	D	0.24	0/2198	0.40	0/2964
9	E	0.25	0/1260	0.40	0/1694
10	F	0.25	0/1821	0.38	0/2451
11	G	0.24	0/1816	0.41	0/2450
12	H	0.24	0/1514	0.42	0/2039
13	J	0.24	0/1374	0.43	0/1842
14	L	0.24	0/1524	0.41	0/2046
15	M	0.23	0/1074	0.40	0/1446
16	N	0.23	0/1757	0.41	0/2354
17	O	0.24	0/1585	0.38	0/2128
18	P	0.24	0/1401	0.41	0/1881
19	Q	0.25	0/1050	0.42	0/1419
20	R	0.23	0/1275	0.39	0/1702
21	S	0.24	0/1473	0.41	0/1980
22	T	0.24	0/918	0.41	0/1229
23	U	0.25	0/790	0.43	0/1069
24	V	0.25	0/1018	0.42	0/1369
25	W	0.24	0/1918	0.41	0/2586
26	X	0.24	0/952	0.40	0/1285
27	Y	0.23	0/1004	0.39	0/1341
28	Z	0.24	0/1118	0.41	0/1497
29	a	0.25	0/751	0.39	0/1013
30	b	0.24	0/3764	0.40	0/5075
31	c	0.24	0/751	0.39	0/1008
32	d	0.23	0/870	0.39	0/1168

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	e	0.23	0/1041	0.40	0/1394
34	f	0.25	0/868	0.42	0/1168
35	g	0.23	0/891	0.42	0/1191
36	h	0.24	0/978	0.39	0/1301
37	i	0.24	0/778	0.38	0/1034
38	j	0.25	0/696	0.42	0/923
39	k	0.25	0/567	0.42	0/754
40	l	0.24	0/443	0.41	0/588
41	m	0.23	0/3848	0.41	0/5181
42	p	0.24	0/672	0.45	0/895
43	r	0.24	0/1892	0.42	0/2528
44	s	0.24	0/448	0.39	0/585
45	u	0.24	0/1287	0.38	0/1711
46	v	0.24	0/2361	0.40	0/3153
47	w	0.23	0/1471	0.40	0/1980
48	x	0.23	0/3897	0.41	0/5282
49	y	0.23	0/1872	0.43	0/2548
50	z	0.24	0/336	0.33	0/443
All	All	0.20	0/146137	0.62	54/213233 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
41	m	0	1

There are no bond length outliers.

The worst 5 of 54 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	3	98	C	C2-N1-C1'	7.20	126.72	118.80
1	1	1082	U	OP1-P-OP2	-6.81	109.39	119.60
1	1	2376	G	OP1-P-OP2	-6.80	109.39	119.60
1	1	3157	U	OP1-P-OP2	-6.80	109.40	119.60
1	1	2943	G	OP1-P-OP2	-6.80	109.41	119.60

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
41	m	77	TRP	Peptide

5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	5	71/120 (59%)	71 (100%)	0	0	100	100
5	A	194/254 (76%)	187 (96%)	7 (4%)	0	100	100
6	B	384/387 (99%)	362 (94%)	22 (6%)	0	100	100
7	C	348/362 (96%)	323 (93%)	24 (7%)	1 (0%)	41	72
8	D	263/297 (89%)	248 (94%)	15 (6%)	0	100	100
9	E	152/176 (86%)	145 (95%)	7 (5%)	0	100	100
10	F	220/244 (90%)	215 (98%)	5 (2%)	0	100	100
11	G	226/256 (88%)	213 (94%)	13 (6%)	0	100	100
12	H	186/191 (97%)	178 (96%)	8 (4%)	0	100	100
13	J	167/174 (96%)	155 (93%)	12 (7%)	0	100	100
14	L	185/199 (93%)	169 (91%)	16 (9%)	0	100	100
15	M	135/138 (98%)	131 (97%)	4 (3%)	0	100	100
16	N	201/204 (98%)	193 (96%)	8 (4%)	0	100	100
17	O	195/199 (98%)	195 (100%)	0	0	100	100
18	P	170/184 (92%)	166 (98%)	4 (2%)	0	100	100
19	Q	132/186 (71%)	130 (98%)	2 (2%)	0	100	100
20	R	154/189 (82%)	153 (99%)	1 (1%)	0	100	100
21	S	169/172 (98%)	160 (95%)	9 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
22	T	105/160 (66%)	96 (91%)	9 (9%)	0	100	100
23	U	96/121 (79%)	95 (99%)	1 (1%)	0	100	100
24	V	134/137 (98%)	133 (99%)	1 (1%)	0	100	100
25	W	232/236 (98%)	223 (96%)	9 (4%)	0	100	100
26	X	115/142 (81%)	112 (97%)	3 (3%)	0	100	100
27	Y	124/127 (98%)	122 (98%)	2 (2%)	0	100	100
28	Z	133/136 (98%)	125 (94%)	8 (6%)	0	100	100
29	a	91/149 (61%)	89 (98%)	2 (2%)	0	100	100
30	b	449/647 (69%)	421 (94%)	28 (6%)	0	100	100
31	c	95/105 (90%)	94 (99%)	1 (1%)	0	100	100
32	d	103/113 (91%)	100 (97%)	3 (3%)	0	100	100
33	e	125/130 (96%)	122 (98%)	3 (2%)	0	100	100
34	f	104/107 (97%)	98 (94%)	6 (6%)	0	100	100
35	g	110/121 (91%)	109 (99%)	1 (1%)	0	100	100
36	h	117/120 (98%)	109 (93%)	7 (6%)	1 (1%)	17	49
37	i	97/100 (97%)	91 (94%)	6 (6%)	0	100	100
38	j	85/88 (97%)	84 (99%)	1 (1%)	0	100	100
39	k	64/78 (82%)	64 (100%)	0	0	100	100
40	l	48/51 (94%)	48 (100%)	0	0	100	100
41	m	465/486 (96%)	429 (92%)	35 (8%)	1 (0%)	47	78
42	p	85/92 (92%)	80 (94%)	5 (6%)	0	100	100
43	r	224/261 (86%)	206 (92%)	18 (8%)	0	100	100
44	s	50/520 (10%)	47 (94%)	3 (6%)	0	100	100
45	u	148/199 (74%)	143 (97%)	5 (3%)	0	100	100
46	v	283/344 (82%)	277 (98%)	6 (2%)	0	100	100
47	w	178/203 (88%)	168 (94%)	10 (6%)	0	100	100
48	x	476/515 (92%)	456 (96%)	20 (4%)	0	100	100
49	y	242/245 (99%)	236 (98%)	6 (2%)	0	100	100
50	z	40/106 (38%)	38 (95%)	2 (5%)	0	100	100
All	All	8170/9771 (84%)	7809 (96%)	358 (4%)	3 (0%)	100	100

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
36	h	91	ALA
41	m	78	PHE
7	C	131	VAL

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	5	67/106 (63%)	66 (98%)	1 (2%)	65	82
5	A	155/196 (79%)	154 (99%)	1 (1%)	86	94
6	B	322/323 (100%)	316 (98%)	6 (2%)	57	78
7	C	283/289 (98%)	278 (98%)	5 (2%)	59	79
8	D	223/245 (91%)	221 (99%)	2 (1%)	78	90
9	E	134/153 (88%)	134 (100%)	0	100	100
10	F	186/205 (91%)	185 (100%)	1 (0%)	88	94
11	G	187/208 (90%)	180 (96%)	7 (4%)	34	62
12	H	168/171 (98%)	166 (99%)	2 (1%)	71	85
13	J	147/150 (98%)	145 (99%)	2 (1%)	67	83
14	L	149/159 (94%)	148 (99%)	1 (1%)	84	92
15	M	108/109 (99%)	106 (98%)	2 (2%)	57	78
16	N	175/176 (99%)	174 (99%)	1 (1%)	86	94
17	O	160/162 (99%)	158 (99%)	2 (1%)	69	84
18	P	140/146 (96%)	138 (99%)	2 (1%)	67	83
19	Q	110/151 (73%)	108 (98%)	2 (2%)	59	79
20	R	129/154 (84%)	127 (98%)	2 (2%)	62	81
21	S	155/156 (99%)	152 (98%)	3 (2%)	57	78
22	T	99/137 (72%)	96 (97%)	3 (3%)	41	68
23	U	85/107 (79%)	84 (99%)	1 (1%)	71	85
24	V	104/105 (99%)	103 (99%)	1 (1%)	76	88
25	W	211/213 (99%)	207 (98%)	4 (2%)	57	78

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
26	X	102/118 (86%)	101 (99%)	1 (1%)	76	88
27	Y	109/110 (99%)	108 (99%)	1 (1%)	78	90
28	Z	115/116 (99%)	114 (99%)	1 (1%)	78	90
29	a	76/119 (64%)	75 (99%)	1 (1%)	69	84
30	b	409/573 (71%)	400 (98%)	9 (2%)	52	75
31	c	81/88 (92%)	80 (99%)	1 (1%)	71	85
32	d	92/97 (95%)	92 (100%)	0	100	100
33	e	109/111 (98%)	109 (100%)	0	100	100
34	f	90/91 (99%)	90 (100%)	0	100	100
35	g	95/103 (92%)	94 (99%)	1 (1%)	73	86
36	h	104/105 (99%)	104 (100%)	0	100	100
37	i	81/82 (99%)	80 (99%)	1 (1%)	71	85
38	j	70/71 (99%)	70 (100%)	0	100	100
39	k	63/69 (91%)	62 (98%)	1 (2%)	62	81
40	l	45/46 (98%)	43 (96%)	2 (4%)	28	58
41	m	413/428 (96%)	403 (98%)	10 (2%)	49	74
42	p	68/72 (94%)	66 (97%)	2 (3%)	42	69
43	r	203/229 (89%)	199 (98%)	4 (2%)	55	77
44	s	48/445 (11%)	45 (94%)	3 (6%)	18	47
45	u	133/180 (74%)	130 (98%)	3 (2%)	50	74
46	v	258/309 (84%)	256 (99%)	2 (1%)	81	91
47	w	161/179 (90%)	156 (97%)	5 (3%)	40	68
48	x	428/451 (95%)	421 (98%)	7 (2%)	62	81
49	y	210/211 (100%)	207 (99%)	3 (1%)	67	83
50	z	36/95 (38%)	36 (100%)	0	100	100
All	All	7096/8319 (85%)	6987 (98%)	109 (2%)	66	82

5 of 109 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
30	b	48	ARG
41	m	30	TYR
48	x	20	ARG

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Mol	Chain	Res	Type
30	b	169	THR
35	g	102	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 36 such sidechains are listed below:

Mol	Chain	Res	Type
45	u	82	ASN
49	y	82	GLN
46	v	9	ASN
48	x	116	GLN
13	J	150	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	2987/3396 (87%)	579 (19%)	80 (2%)
2	2	153/158 (96%)	25 (16%)	2 (1%)
3	3	120/121 (99%)	17 (14%)	1 (0%)
All	All	3260/3675 (88%)	621 (19%)	83 (2%)

5 of 621 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	13	A
1	1	14	U
1	1	20	A
1	1	26	A
1	1	40	A

5 of 83 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	2728	G
1	1	3078	U
1	1	2761	G
1	1	2869	U
1	1	3228	C

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 5 ligands modelled in this entry, 5 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

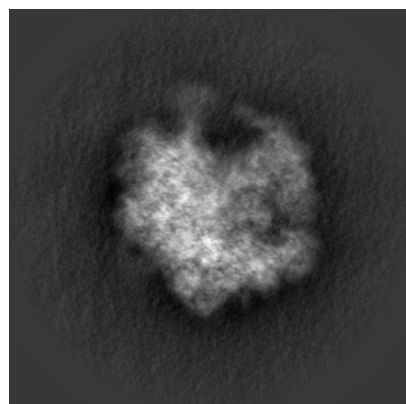
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-12892. These allow visual inspection of the internal detail of the map and identification of artifacts.

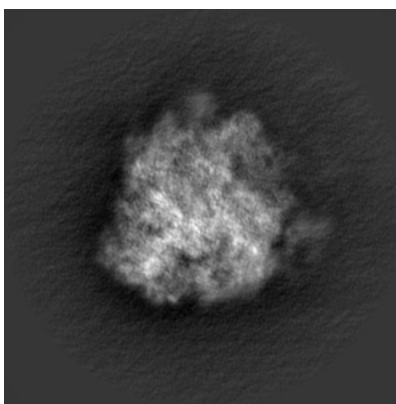
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

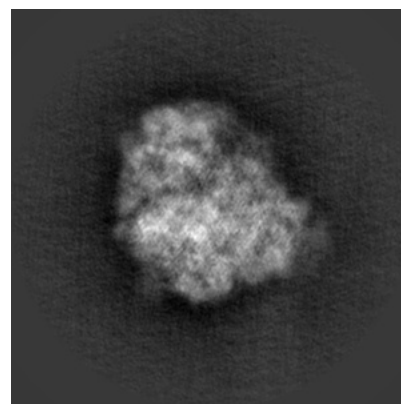
6.1.1 Primary map



X

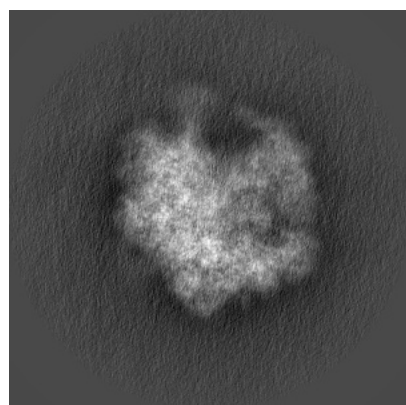


Y

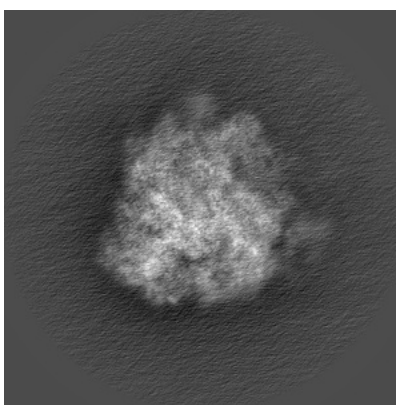


Z

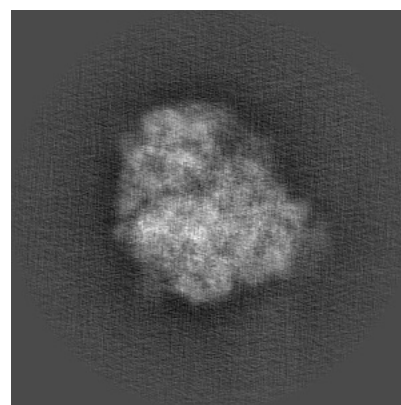
6.1.2 Raw map



X



Y

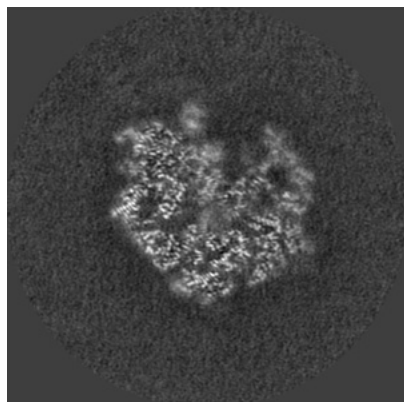


Z

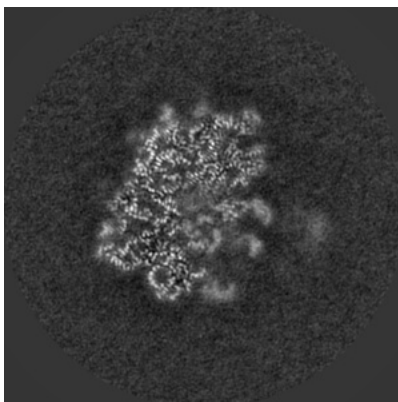
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

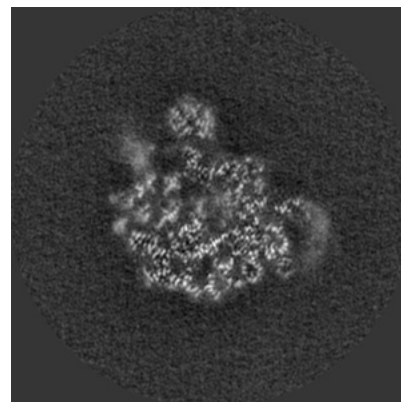
6.2.1 Primary map



X Index: 200

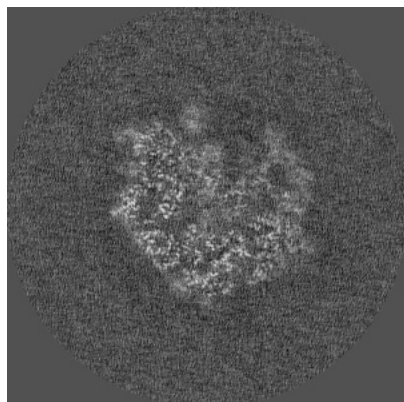


Y Index: 200

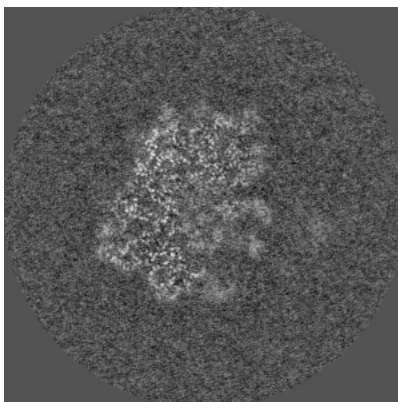


Z Index: 200

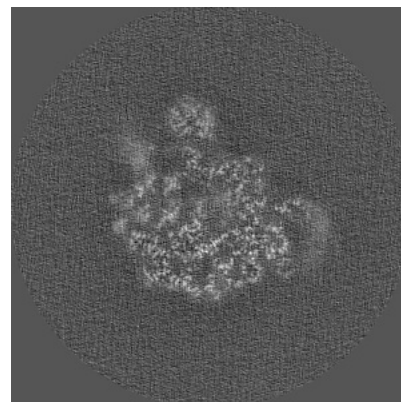
6.2.2 Raw map



X Index: 200



Y Index: 200

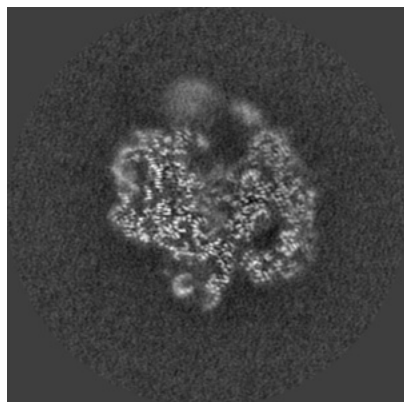


Z Index: 200

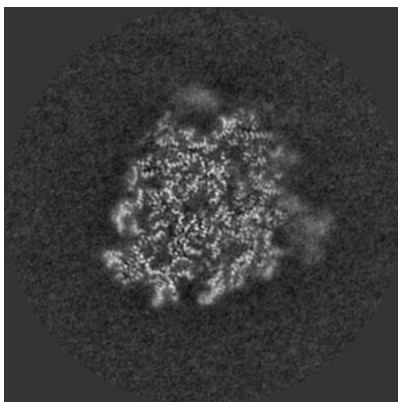
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

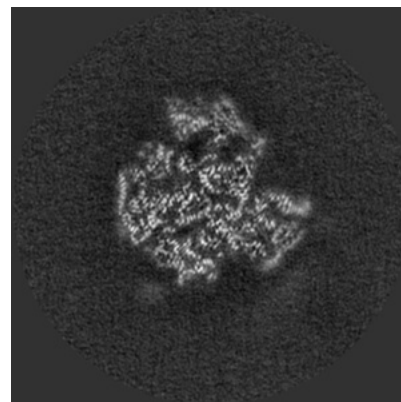
6.3.1 Primary map



X Index: 184

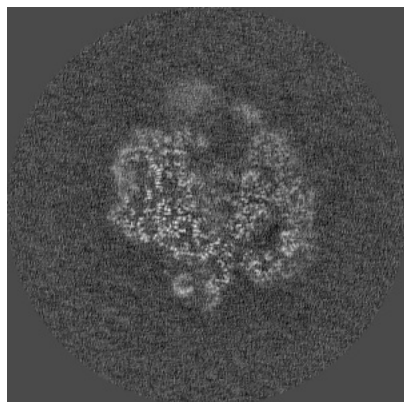


Y Index: 177

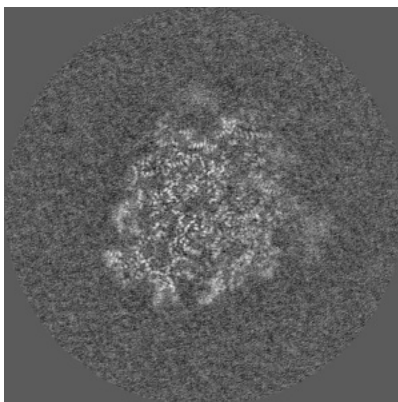


Z Index: 166

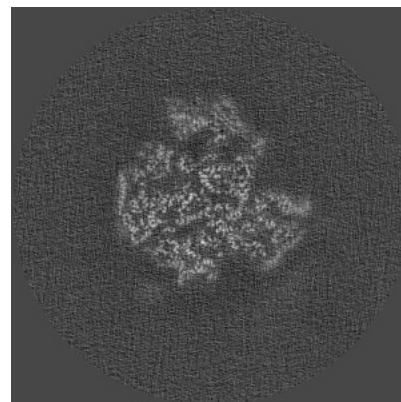
6.3.2 Raw map



X Index: 184



Y Index: 177

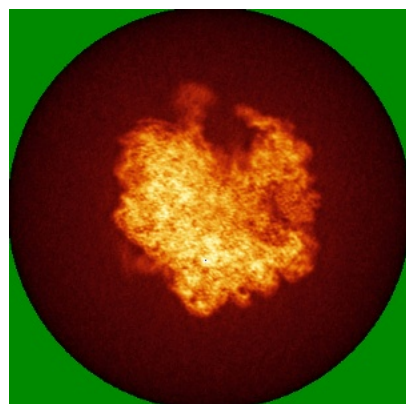


Z Index: 166

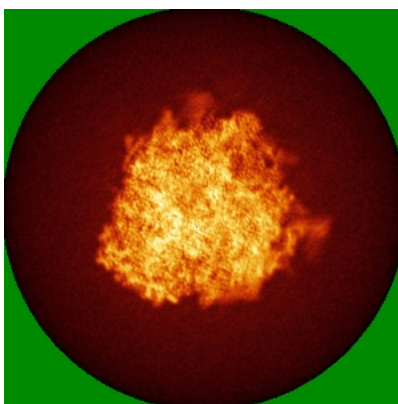
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

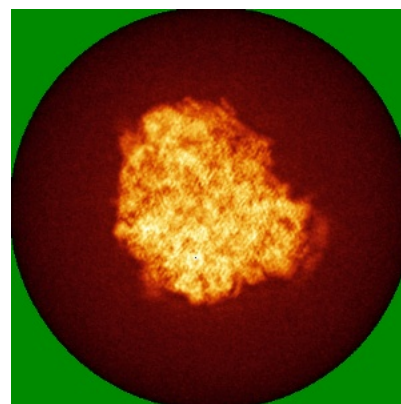
6.4.1 Primary map



X

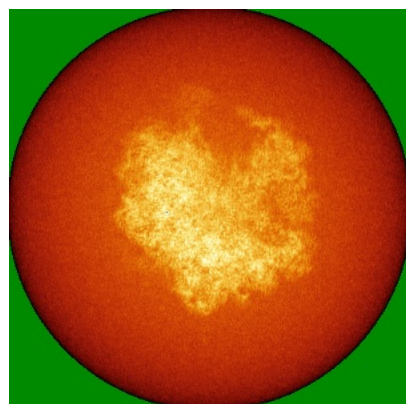


Y

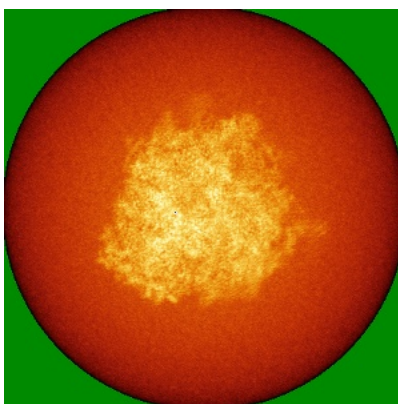


Z

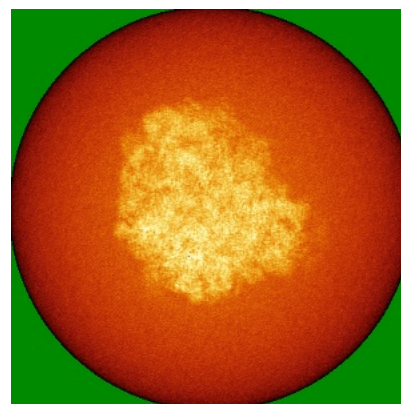
6.4.2 Raw map



X



Y

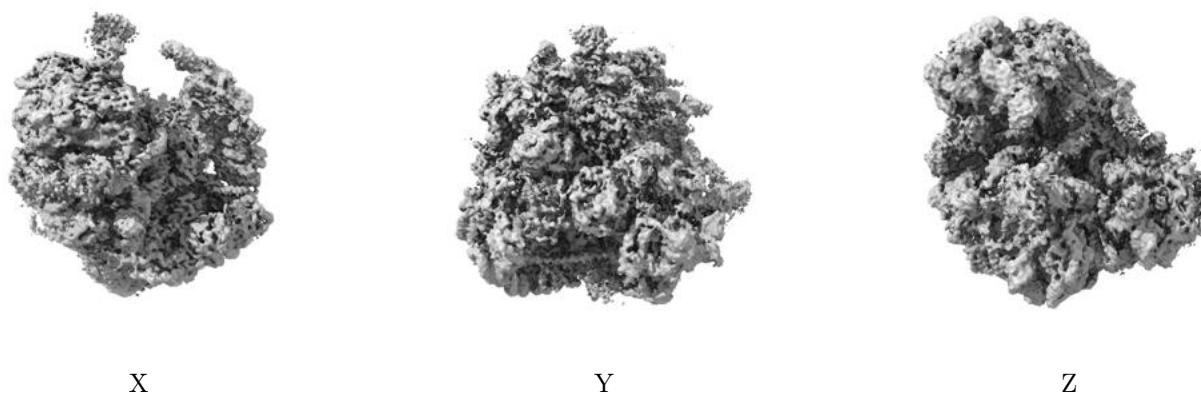


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

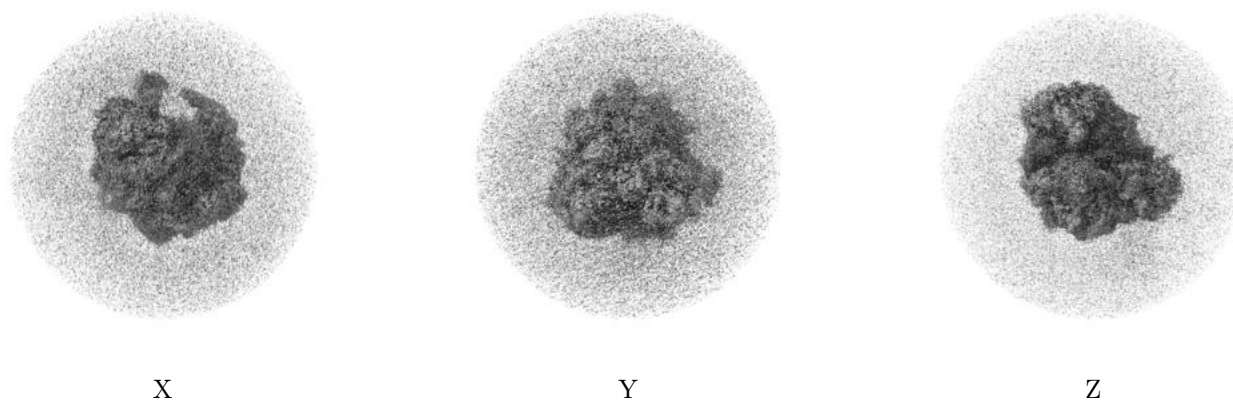
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.026. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

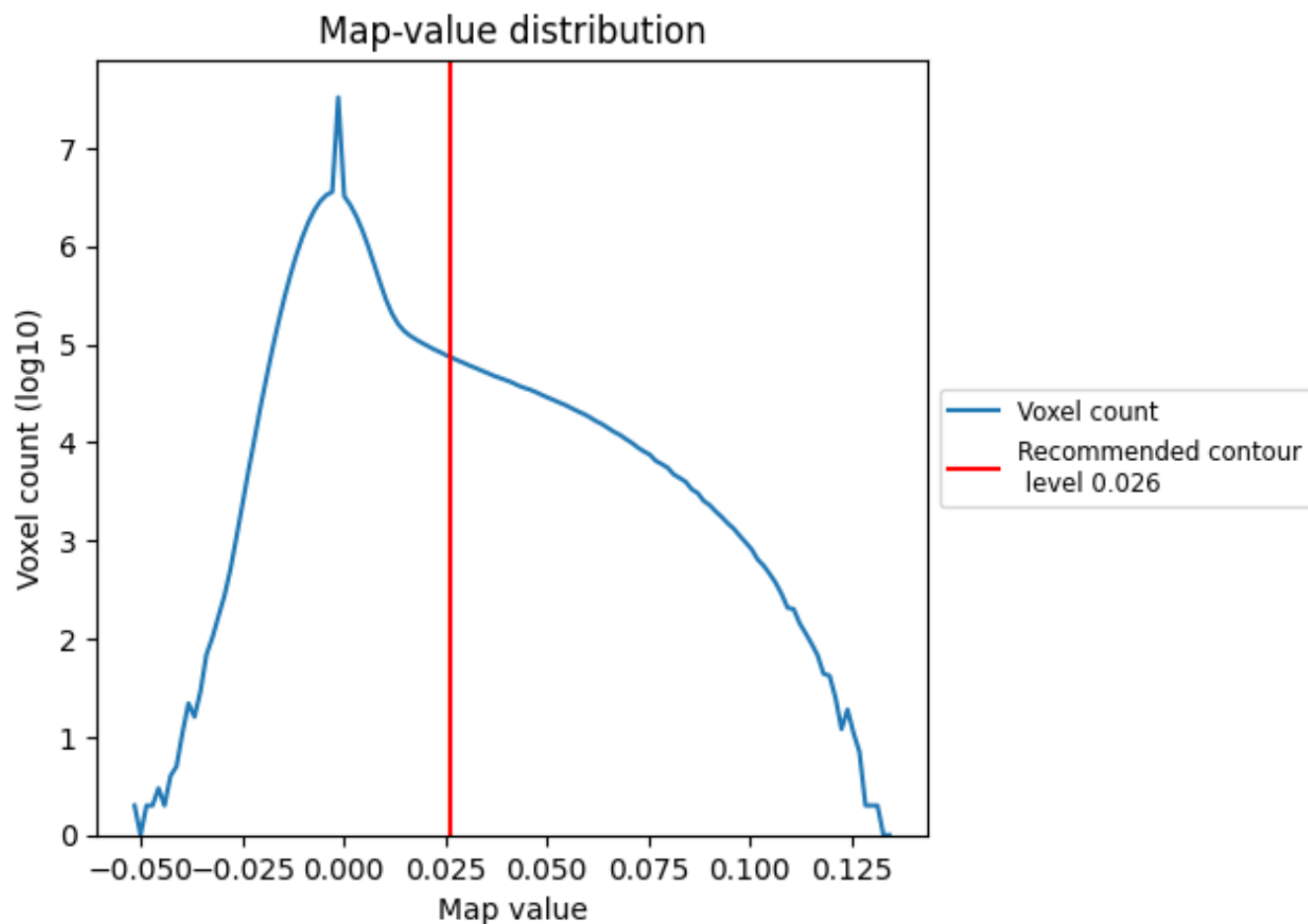
6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

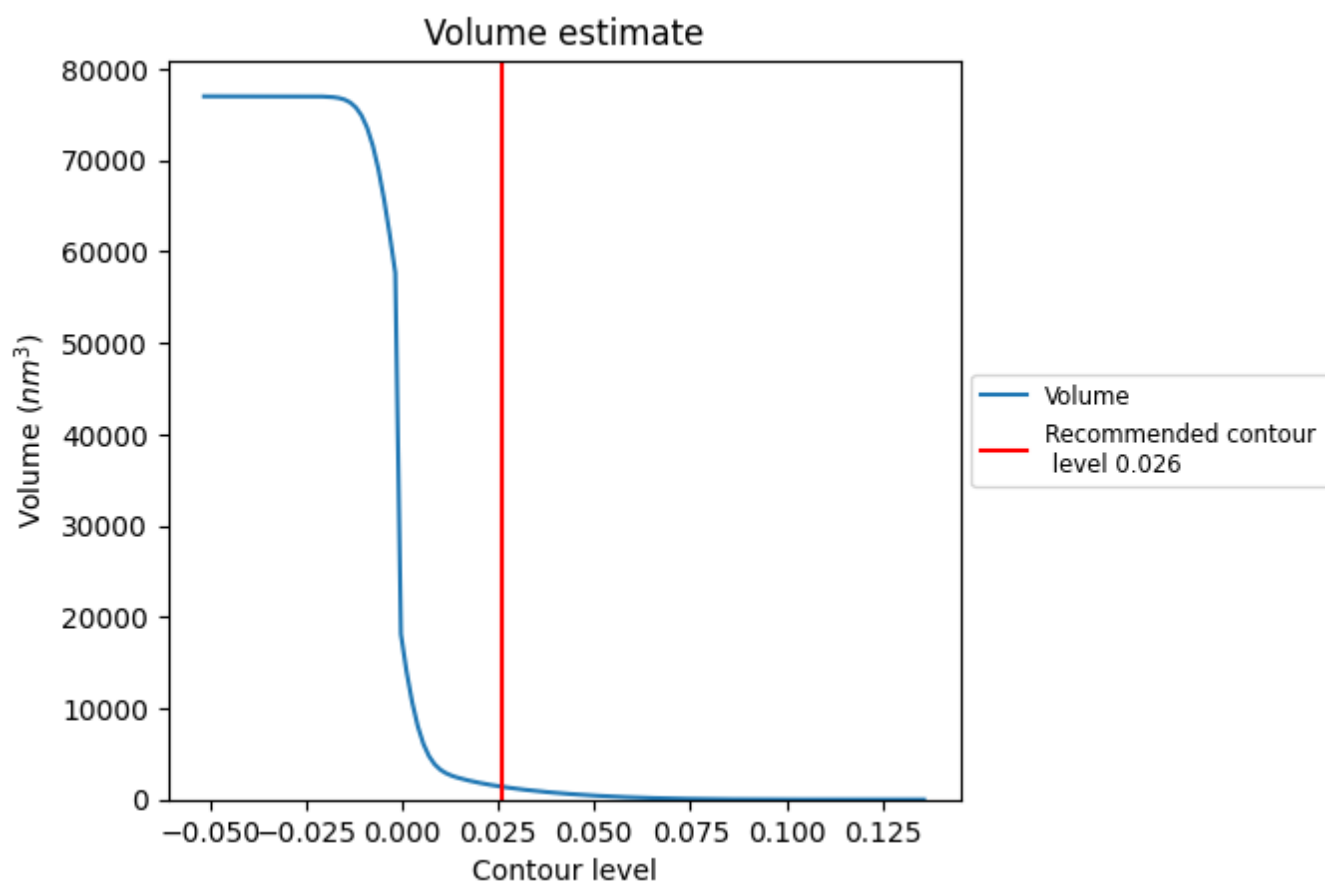
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

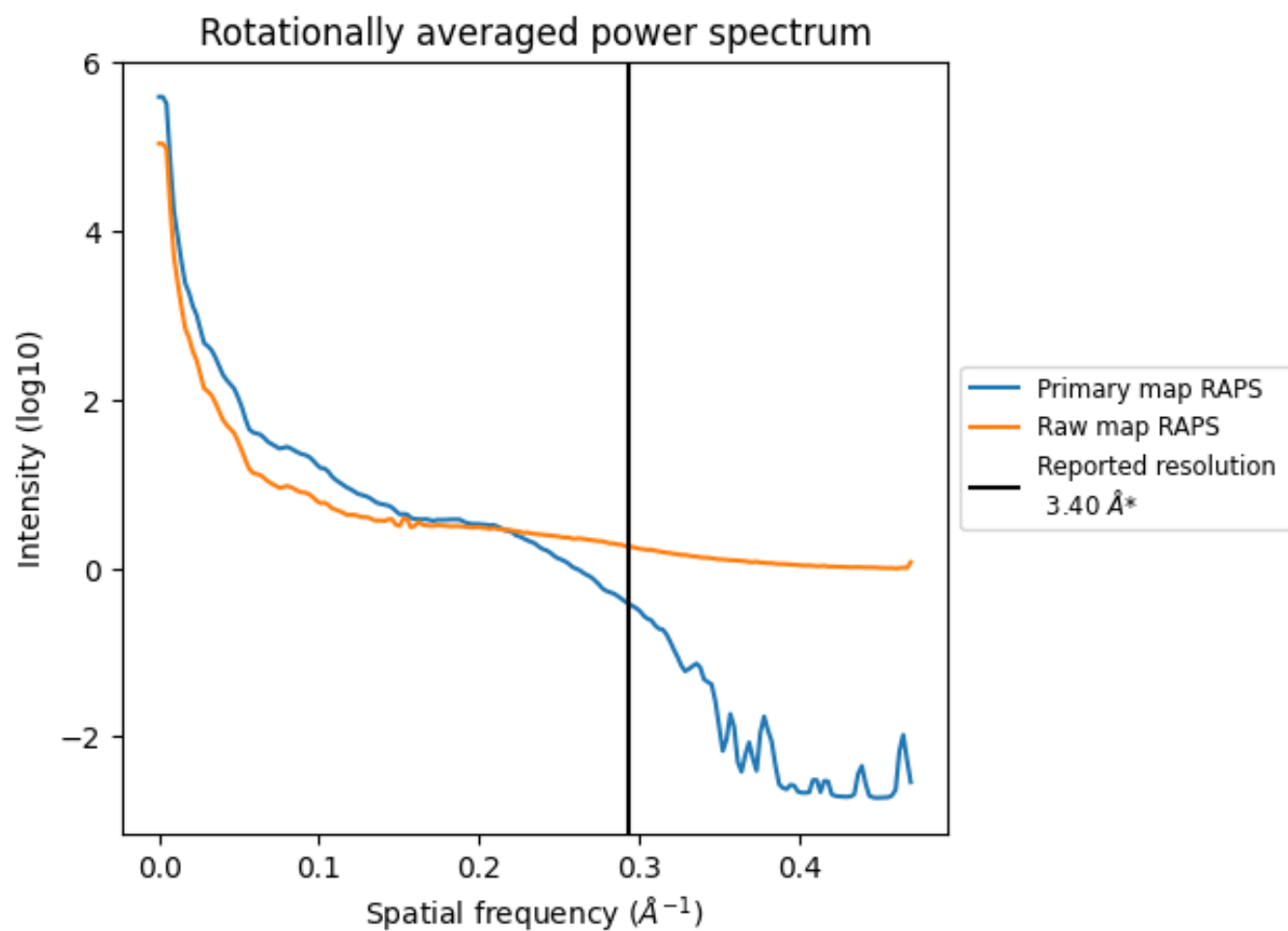
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1405 nm³; this corresponds to an approximate mass of 1269 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

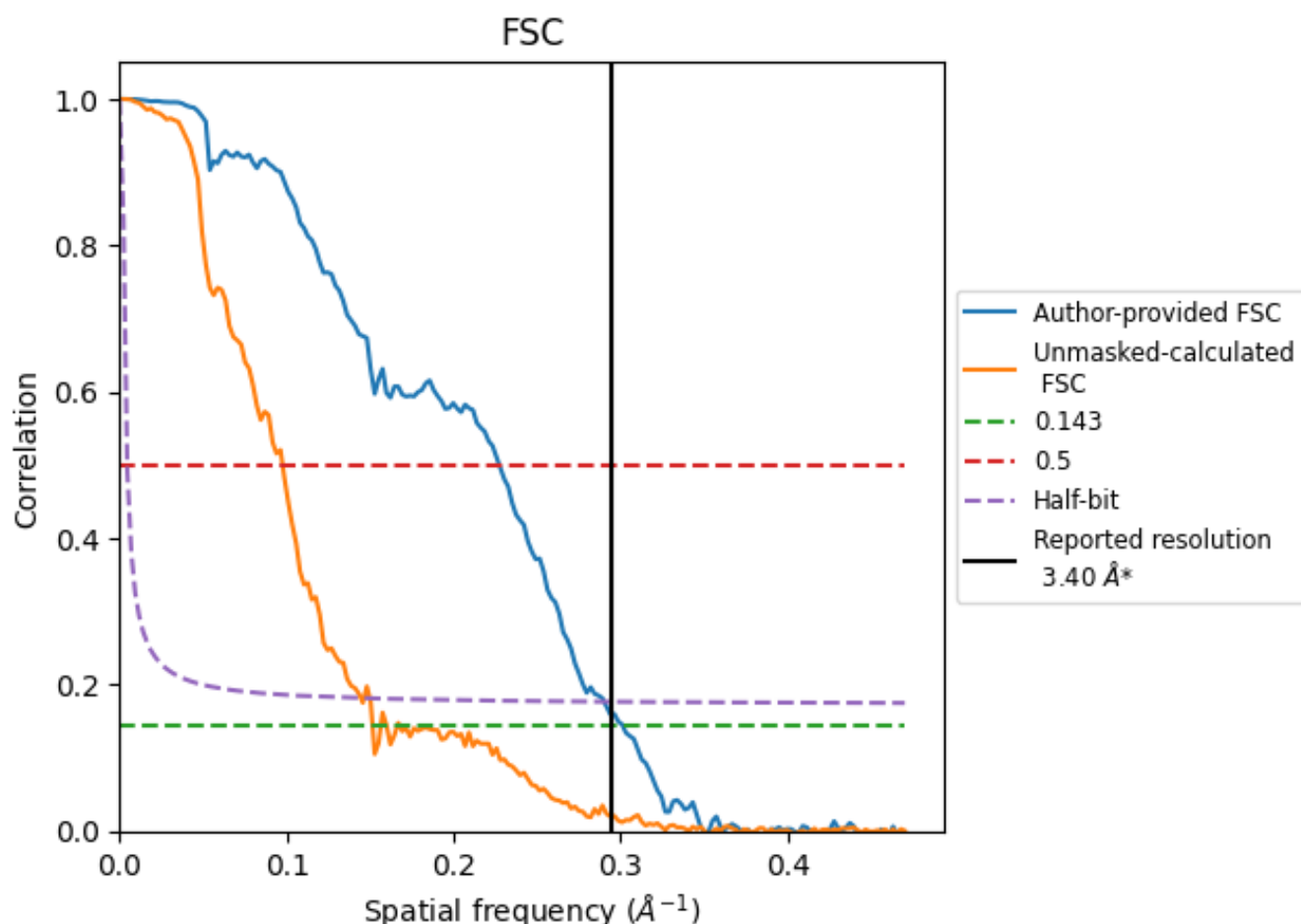


*Reported resolution corresponds to spatial frequency of 0.294 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.294 Å⁻¹

8.2 Resolution estimates [i](#)

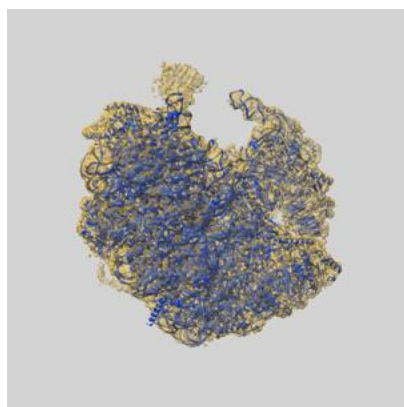
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	3.32	4.40	3.45
Unmasked-calculated*	6.60	10.25	6.92

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 6.60 differs from the reported value 3.4 by more than 10 %

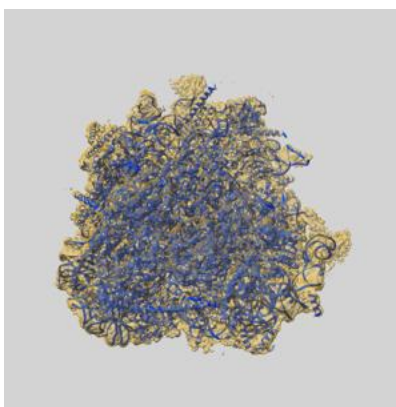
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-12892 and PDB model 7OH3. Per-residue inclusion information can be found in [section 3](#) on [page 13](#).

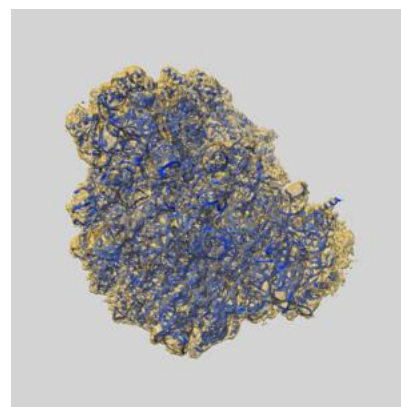
9.1 Map-model overlay [i](#)



X



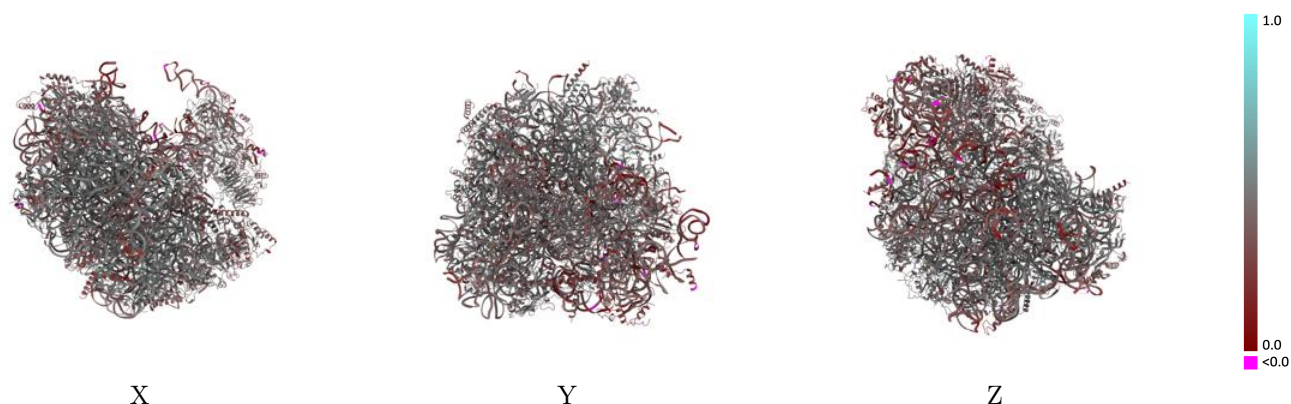
Y



Z

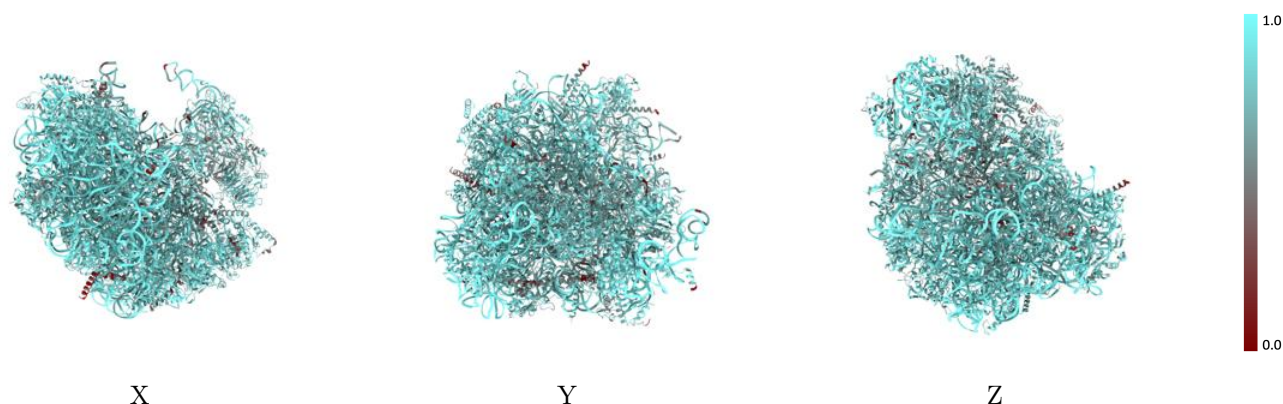
The images above show the 3D surface view of the map at the recommended contour level 0.026 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



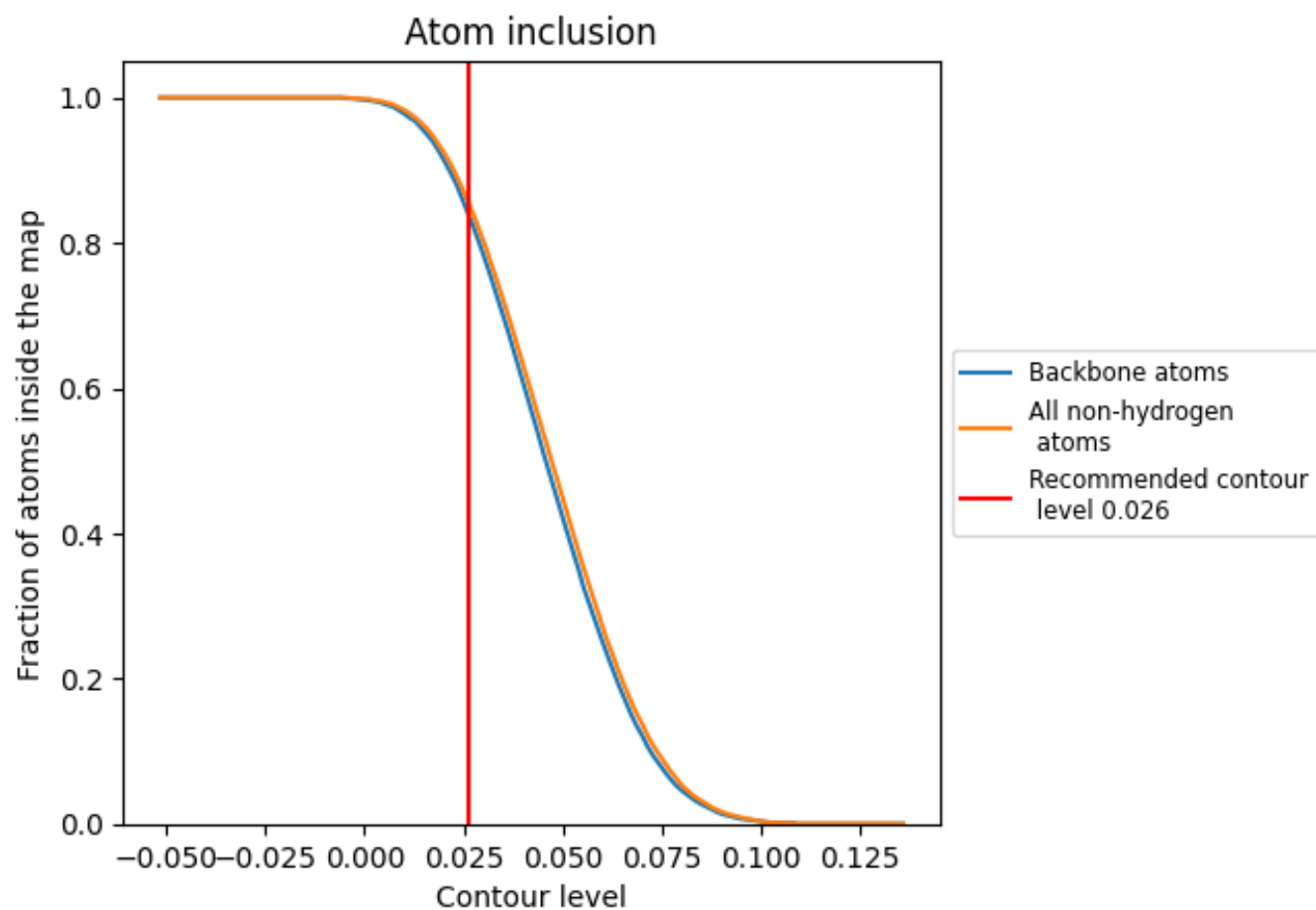
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.026).







































































9.4 Atom inclusion ⓘ



At the recommended contour level, 84% of all backbone atoms, 86% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

































The table lists the average atom inclusion at the recommended contour level (0.026) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8590	 0.4160
1	 0.9230	 0.4070
2	 0.9510	 0.4420
3	 0.9550	 0.3220
5	 0.4720	 0.3130
A	 0.7550	 0.4770
B	 0.8250	 0.4620
C	 0.8300	 0.4630
D	 0.7920	 0.3600
E	 0.8480	 0.4550
F	 0.8430	 0.4540
G	 0.7830	 0.4080
H	 0.8430	 0.4600
J	 0.7690	 0.2890
L	 0.8110	 0.4380
M	 0.8420	 0.4580
N	 0.7780	 0.4590
O	 0.8440	 0.4820
P	 0.8520	 0.4780
Q	 0.8240	 0.4590
R	 0.7930	 0.4550
S	 0.7800	 0.4340
T	 0.7020	 0.4010
U	 0.7790	 0.3840
V	 0.8010	 0.4750
W	 0.8160	 0.3850
X	 0.8310	 0.4630
Y	 0.8590	 0.4650
Z	 0.8170	 0.4220
a	 0.8350	 0.4460
b	 0.7810	 0.4000
c	 0.8500	 0.4350
d	 0.7920	 0.4570
e	 0.7990	 0.4790
f	 0.8340	 0.4980



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Chain	Atom inclusion	Q-score
g	 0.7850	 0.4630
h	 0.8220	 0.4290
i	 0.7800	 0.4250
j	 0.8340	 0.4790
k	 0.5980	 0.3960
l	 0.7370	 0.4650
m	 0.7140	 0.4100
p	 0.7860	 0.4520
r	 0.7490	 0.4400
s	 0.5940	 0.4170
u	 0.7140	 0.3920
v	 0.7620	 0.3950
w	 0.6880	 0.3680
x	 0.7660	 0.3890
y	 0.8110	 0.4350
z	 0.3750	 0.3770